

J. Hunt

1600

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/509,779

CRF Processing Date: 8/28/2001
Edited by: [Signature]
Verified by: [Signature] (STIC sta:)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filenam at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

RAW SEQUENCE LISTING

DATE: 08/28/2001

PATENT APPLICATION: US/09/509,779

TIME: 15:25:19

Input Set : A:\Pto.amc

Output Set: N:\CRF3\08282001\I509779.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: SUN, Yi

8 (ii) TITLE OF INVENTION: SAG: Sensitive to Apoptosis Gene

10 (iii) NUMBER OF SEQUENCES: 50

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Warner-Lambert Company

14 (B) STREET: 2800 Plymouth Road

15 (C) CITY: Ann Arbor

16 (D) STATE: Michigan

17 (E) COUNTRY: USA

18 (F) ZIP: 48105

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

26 (vi) CURRENT APPLICATION DATA:

27 (A) APPLICATION NUMBER: US/09/509,779

28 (B) FILING DATE: 29-Mar-2000

30 (viii) ATTORNEY/AGENT INFORMATION:

31 (A) NAME: David R. Kurlandsky

32 (B) REGISTRATION NUMBER: 41,505

33 (C) REFERENCE/DOCKET NUMBER: 5650-01-DRK

35 (ix) TELECOMMUNICATION INFORMATION:

36 (A) TELEPHONE: 734-622-7304

37 (B) TELEFAX: 734-622-1553

39 (2) INFORMATION FOR SEQ ID NO: 1:

41 (i) SEQUENCE CHARACTERISTICS:

42 (A) LENGTH: 1140 base pairs

43 (B) TYPE: nucleic acid

44 (C) STRANDEDNESS: double

45 (D) TOPOLOGY: linear

47 (ii) MOLECULE TYPE: cDNA

50 (ix) FEATURE:

51 (A) NAME/KEY: CDS

52 (B) LOCATION:17..355

54 (ix) FEATURE:

55 (A) NAME/KEY: mat_peptide

56 (B) LOCATION:17..355

58 (ix) FEATURE:

59 (A) NAME/KEY: misc_feature

60 (B) LOCATION:1..1140

61 (D) OTHER INFORMATION:/note= "Mouse SAG"

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

66 GTTCTGCGCC GCCGCC ATG GCC GAC GTG GAG GAC GGC GAG GAA CCC TGC
67 Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys

49

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68          1          5          10
70 GTC CTT TCT TCG CAC TCC GGG AGC GCA GGC TCC AAG TCG GGA GGC GAC      97
71 Val Leu Ser Ser His Ser Gly Ser Ala Gly Ser Lys Ser Gly Gly Asp
72          15          20          25
74 AAG ATG TTC TCT CTC AAG AAG TGG AAC GCG GTA GCC ATG TGG AGC TGG      145
75 Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp
76          30          35          40
77 GAC GTT GAG TGC GAT ACC TGT GCC ATC TGC AGG GTC CAG GTG ATG GAT      193
78 Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp
79          45          50          55
81 GCC TGC CTT CGA TGT CAA GCT GAA AAC AAG CAA GAG GAC TGT GTT GTG      241
82 Ala Cys Leu Arg Cys Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val
83 60          65          70          75
85 GTC TGG GGA GAG TGT AAC CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG      289
86 Val Trp Gly Glu Cys Asn His Ser Phe His Asn Cys Cys Met Ser Leu
87          80          85          90
89 TGG GTG AAA CAG AAC AAT CGC TGC CCT CTG TGC CAG CAG GAC TGG GTA      337
90 Trp Val Lys Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val
91          95          100          105
93 GTC CAA AGA ATC GGC AAA TGAGAGGTGG CCCAGGCGCT CCTGGTGTGG      385
94 Val Gln Arg Ile Gly Lys
95          110
97 TTGCTGACCC TGGACAAAGA CTAAACACTG CAGGGGATTC ATCCTTGAGA GAGAGAGGAT      445
99 GCTGTGCGCC TTTGAGACTC ACCAAAGGCT TGCTTTATTA ATTTGTCTGT TTAGTTTGG      505
101 GAAATTCTCT ACAATTAAGA TAATTGTTA AAAATGGCCT TTCCTACCTC TGGTGTGTGT      565
103 GTGTGATACG AATGCATAGA AGAGCGAGAA CACCAGAAAA TGATCTTTGT TTATCTGTAC      625
105 CCACGACTGG AACATTGTGT TCACAGAAGA ACATTGTTTG TGTTTATGCT TGAGGGTTAA      685
107 AAAATAGATA AACGAATGTT ACAGTAACAA ATAAAATGCA TTGAAAAGCC GACTCCTCCT      745
109 AATCCTTTTT GTGTTGGGAG AGAGGCAAGC GAGGCCACCC TGCTGTCTTC ATTTGCTGTG      805
111 AATGAGGATT TTAACCTGCA CTCAGTGAAG AGGCGTAACT GTCGGGTAAA CTGTAATATG      865
113 GCGTAACTGT CGGGTAAACG GCTTTGTCTC CTGACTTCTC CATCTTTGAC TTGGCCAGGA      925
115 AGCCTGGATT GTTCAACCAC TTAGTTCTAA AGAACTGTTT TCTGTTTTTG CCGAAGGTTG      985
117 TATTGTATGT TTTAGTCAAA AATATTAGTA GGAAAATGGC TTACTAGTAT AACACTGAAG      1045
119 TTCATTATGC AATGTTTTAA TAAAATATTG TGCTTTGAGT TATTAAAGTT TGATATATAC      1105
121 TCTTAAATC ATTAACTAA TTCATCAATT AAATG      1140
124 (2) INFORMATION FOR SEQ ID NO: 2:
126 (i) SEQUENCE CHARACTERISTICS:
127 (A) LENGTH: 113 amino acids
128 (B) TYPE: amino acid
129 (D) TOPOLOGY: linear
131 (ii) MOLECULE TYPE: protein
132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
134 Met Ala Asp Val Glu Asp Gly Glu Glu Pro Cys Val Leu Ser Ser His
135 1          5          10          15
137 Ser Gly Ser Ala Gly Ser Lys Ser Gly Asp Lys Met Phe Ser Leu
138          20          25          30
140 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
141          35          40          45
143 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys

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144      50      55      60
146 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
147 65      70      75      80
149 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
150      85      90      95
152 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
153      100      105      110
155 Lys
158 (2) INFORMATION FOR SEQ ID NO: 3:
160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 754 base pairs
162 (B) TYPE: nucleic acid
163 (C) STRANDEDNESS: double
164 (D) TOPOLOGY: linear
166 (ii) MOLECULE TYPE: cDNA
169 (ix) FEATURE:
170 (A) NAME/KEY: CDS
171 (B) LOCATION:1..339
173 (ix) FEATURE:
174 (A) NAME/KEY: mat_peptide
175 (B) LOCATION:1..339
177 (ix) FEATURE:
178 (A) NAME/KEY: misc_feature
179 (B) LOCATION:1..754
180 (D) OTHER INFORMATION:/note= "Human SAG"
183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
185 ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC TGC GCC CTG GCC TCT CAC      48
186 Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
187 1      5      10      15
189 TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC GAC AAG ATG TTC TCC CTC      96
190 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
191      20      25      30
193 AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC TGG GAC GTG GAG TGC GAT      144
194 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
195      35      40      45
197 ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG GAT GCC TGT CTT AGA TGT      192
198 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
199      50      55      60
201 CAA GCT GAA AAC AAA CAA GAG GAC TGT GTT GTG GTC TGG GGA GAA TGT      240
202 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
203 65      70      75      80
205 AAT CAT TCC TTC CAC AAC TGC TGC ATG TCC CTG TGG GTG AAA CAG AAC      288
206 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
207      85      90      95
209 AAT CGC TGC CCT CTC TGC CAG CAG GAC TGG GTG GTC CAA AGA ATC GGC      336
210 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
211      100      105      110
213 AAA TGAGAGTGGT TAGAAGGCTT CTTAGCGCAG TTGTTTCAGAG CCCTGGTGGA      389
214 Lys

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```

217 TCTTGTAATC CAGTGCCCTA CAAAGGCTAG AACACTACAG GGGATGAATT CTTCAAATAG      449
219 GAGCCGATGG ATCTGTGGTC TTTGGACTCA TCAAAGCCTT GGTTAGCATT TGTCAGTTTT      509
221 ATCTTCAGAA ATTCTCTGTG ATTAAGAAGA TAATTTATTA AAGGTGGTCC TTCCTACCTC      569
223 TGTGGTGTGT GTCGCGCACA CAGCTTAGAA GTGCTATAAA AAAGGAAAGA GCTCCAAATT      629
225 GAATCACCTT ATAATTTACC CATTTCTATA CAACAGGCAG TGGAAGCAGT TTCGAGACTT      689
227 TTTCGATGCT TATGGTTGAT CAGTTAAAAA AGAATGTTAC AGTAACAAAT AAAGTGCAGT      749
229 TTAATA                                     754

```

232 (2) INFORMATION FOR SEQ ID NO: 4:

234 (i) SEQUENCE CHARACTERISTICS:

235 (A) LENGTH: 113 amino acids

236 (B) TYPE: amino acid

237 (D) TOPOLOGY: linear

239 (ii) MOLECULE TYPE: protein

240 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

242 Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
243   1           5           10           15
245 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
246           20           25           30
248 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
249           35           40           45
251 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Leu Arg Cys
252           50           55           60
254 Gln Ala Glu Asn Lys Gln Glu Asp Cys Val Val Val Trp Gly Glu Cys
255   65           70           75           80
257 Asn His Ser Phe His Asn Cys Cys Met Ser Leu Trp Val Lys Gln Asn
258           85           90           95
260 Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg Ile Gly
261           100          105          110
263 Lys

```

266 (2) INFORMATION FOR SEQ ID NO: 5:

268 (i) SEQUENCE CHARACTERISTICS:

269 (A) LENGTH: 18 base pairs

270 (B) TYPE: nucleic acid

271 (C) STRANDEDNESS: single

272 (D) TOPOLOGY: linear

274 (ii) MOLECULE TYPE: other nucleic acid

```

275 (A) DESCRIPTION: /desc = "oligonucleotide P1
W--> 276 downstream primer"

```

281 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

283 AAGCTTTTTT TTTTTTTR

18

285 (2) INFORMATION FOR SEQ ID NO: 6:

287 (i) SEQUENCE CHARACTERISTICS:

288 (A) LENGTH: 13 base pairs

289 (B) TYPE: nucleic acid

290 (C) STRANDEDNESS: single

291 (D) TOPOLOGY: linear

293 (ii) MOLECULE TYPE: other nucleic acid

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294 (A) DESCRIPTION: /desc = "Oligonucleotide: P2
W--> 295 upstream primer"

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300 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
302 AAGCTTNNNN NNN 13
304 (2) INFORMATION FOR SEQ ID NO: 7:
306 (i) SEQUENCE CHARACTERISTICS:
307 (A) LENGTH: 25 base pairs
308 (B) TYPE: nucleic acid
309 (C) STRANDEDNESS: single
310 (D) TOPOLOGY: linear
312 (ii) MOLECULE TYPE: other nucleic acid
313 (A) DESCRIPTION: /desc = "Oligonucleotide SAG TA.01"
318 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
320 CGGGATCCCC ATGGCCGACG TGAGG 25
322 (2) INFORMATION FOR SEQ ID NO: 8:
324 (i) SEQUENCE CHARACTERISTICS:
325 (A) LENGTH: 26 base pairs
326 (B) TYPE: nucleic acid
327 (C) STRANDEDNESS: single
328 (D) TOPOLOGY: linear
330 (ii) MOLECULE TYPE: other nucleic acid
331 (A) DESCRIPTION: /desc = "oligonucleotide SAG T.02"
336 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
338 CGGGATCCTC ATTTGCCGAT TCTTTG 26
340 (2) INFORMATION FOR SEQ ID NO: 9:
342 (i) SEQUENCE CHARACTERISTICS:
343 (A) LENGTH: 26 base pairs
344 (B) TYPE: nucleic acid
345 (C) STRANDEDNESS: single
346 (D) TOPOLOGY: linear
348 (ii) MOLECULE TYPE: other nucleic acid
349 (A) DESCRIPTION: /desc = "oligonucleotide P.01"
354 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
356 TATGGCTAGC ATGGCCGACG TGGAGG 26
358 (2) INFORMATION FOR SEQ ID NO: 10:
360 (i) SEQUENCE CHARACTERISTICS:
361 (A) LENGTH: 16 amino acids
362 (B) TYPE: amino acid
363 (C) STRANDEDNESS: single
364 (D) TOPOLOGY: linear
366 (ii) MOLECULE TYPE: peptide
371 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
373 Gln Asn Asn Arg Cys Pro Leu Cys Gln Gln Asp Trp Val Val Gln Arg
374 1 5 10 15
377 (2) INFORMATION FOR SEQ ID NO: 11:
379 (i) SEQUENCE CHARACTERISTICS:
380 (A) LENGTH: 747 base pairs
381 (B) TYPE: nucleic acid
382 (C) STRANDEDNESS: double
383 (D) TOPOLOGY: linear
385 (ii) MOLECULE TYPE: cDNA

```

VERIFICATION SUMMARY

DATE: 08/28/2001

PATENT APPLICATION: US/09/509,779

TIME: 15:25:20

Input Set : A:\Pto.amc

Output Set: N:\CRF3\08282001\I509779.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]